

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Lester, Henry A., et al.

(ii) TITLE OF INVENTION: DNA ENCODING INWARD RECTIFIER, G-PROTEIN
ACTIVATED, MAMMALIAN, POTASSIUM KGA CHANNEL

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Cooper & Dunham

(B) STREET: 30 Rockefeller Plaza

(C) CITY: New York

(D) STATE: New York

(E) COUNTRY: USA

(F) ZIP: 10112

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US Not Yet Known

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: White, John P.

(B) REGISTRATION NUMBER: 28,678

(C) REFERENCE/DOCKET NUMBER: 43717/JPW/TEP

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 977-9550

(B) TELEFAX: (212) 664-0525

(C) TELEX: 422523 COOP UI

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 32..1534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGAA TCTGGATCTC CCCTCCGTAT T ATG TCT GCA CTC CGA AGG AAA	52
Met Ser Ala Leu Arg Arg Lys	
1 5	
TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC	100
Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Ser Gly Ser Gly	
10 15 20	
TTG CAG CCC CAG GGG CCA GGA CAG GGC CCA CAG CAG CAG CTT GTA CCC	148
Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro	
25 30 35	
AAG AAG AAA CGG CAG CGG TTC GTG GAC AAG AAC GGT CGG TGC AAT GTG	196
Lys Lys Lys Arg Gln Arg Phe Val Asp Lys Asn Gly Arg Cys Asn Val	
40 45 50 55	
CAG CAC GGC AAC CTG GGC AGC GAG ACC AGT CGC TAC CTT TCC GAC CTC	244
Gln His Gly Asn Leu Gly Ser Glu Thr Ser Arg Tyr Leu Ser Asp Leu	
60 65 70	
TTC ACT ACC CTG GTG GAT CTC AAG TGG CGT TGG AAC CTC TTT ATC TTC	292
Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Trp Asn Leu Phe Ile Phe	
75 80 85	

ATC CTC ACC TAC ACC GTG GCC TGG CTC TTC ATG GCG TCC ATG TGG TGG	340
Ile Leu Thr Tyr Thr Val Ala Trp Leu Phe Met Ala Ser Met Trp Trp	
90 95 100	
GTG ATC GCT TAT ACC CGG GGC GAC CTG AAC AAA GCC CAT GTC GGC AAC	388
Val Ile Ala Tyr Thr Arg Gly Asp Leu Asn Lys Ala His Val Gly Asn	
105 110 115	
TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC CCC TCT GCC TTC CTT	436
Tyr Thr Pro Cys Val Ala Asn Val Tyr Asn Phe Pro Ser Ala Phe Leu	
120 125 130 135	
TTC TTC ATC GAG ACC GAG GCC ACC ATC GGC TAT GGC TAC CGC TAC ATC	484
Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr Arg Tyr Ile	
140 145 150	
ACC GAC AAG TGC CCC GAG GGC ATC ATC CTT TTC CTT TTC CAG TCC ATC	532
Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Phe Leu Phe Gln Ser Ile	
155 160 165	
CTT GGC TCC ATC GTG GAC GCT TTC CTC ATC GGC TGC ATG TTC ATC AAG	580
Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys	
170 175 180	
ATG TCC CAG CCC AAA AAG CGC GCC GAG ACC CTC ATG TTT AGC GAG CAT	628
Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His	
185 190 195	
GCG GTT ATT TCC ATG AGG GAC GGA AAA CTC ACT CTC ATG TTC CGG GTG	676
Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val	
200 205 210 215	
GGC AAC CTG CGC AAC AGC CAC ATG GTC TCC GCG CAG ATC CGC TGC AAG	724
Gly Asn Leu Arg Asn Ser His Met Val Ser Ala Gln Ile Arg Cys Lys	
220 225 230	
CTG CTC AAA TCT CGG CAG ACA CCT GAG GGT GAG TTT CTA CCC CTT GAC	772
Leu Leu Lys Ser Arg Gln Thr Pro Glu Gly Glu Phe Leu Pro Leu Asp	
235 240 245	
CAA CTT GAA CTG GAT GTA GGT TTT AGT ACA GGG GCA GAT CAA CTT TTT	820

Gln Leu Glu Leu Asp Val Gly Phe Ser Thr Gly Ala Asp Gln Leu Phe	
250 255 260	
CTT GTG TCC CCT CTC ACC ATT TGC CAC GTG ATC GAT GCC AAA AGC CCC	868
Leu Val Ser Pro Leu Thr Ile Cys His Val Ile Asp Ala Lys Ser Pro	
265 270 275	
TTT TAT GAC CTA TCC CAG CGA AGC ATG CAA ACT GAA CAG TTC GAG GTG	916
Phe Tyr Asp Leu Ser Gln Arg Ser Met Gln Thr Glu Gln Phe Glu Val	
280 285 290 295	
GTC GTC ATC CTG GAA GGC ATC GTG GAA ACC ACA GGG ATG ACT TGT CAA	964
Val Val Ile Leu Glu Gly Ile Val Glu Thr Thr Gly Met Thr Cys Gln	
300 305 310	
GCT CGA ACA TCA TAC ACC GAA GAT GAA GTT CTT TGG GGT CAT CGT TTT	1012
Ala Arg Thr Ser Tyr Thr Glu Asp Glu Val Leu Trp Gly His Arg Phe	
315 320 325	
TTC CCT GTA ATT TCT TTA GAA GAA GGA TTC TTT AAA GTC GAT TAC TCC	1060
Phe Pro Val Ile Ser Leu Glu Glu Gly Phe Phe Lys Val Asp Tyr Ser	
330 335 340	
CAG TTC CAT GCA ACC TTT GAA GTC CCC ACC CCT CCG TAC AGT GTG AAA	1108
Gln Phe His Ala Thr Phe Glu Val Pro Thr Pro Pro Tyr Ser Val Lys	
345 350 355	
GAG CAG GAA GAA ATG CTT CTC ATG TCT TCC CCT TTA ATA GCA CCA GCC	1156
Glu Gln Glu Glu Met Leu Leu Met Ser Ser Pro Leu Ile Ala Pro Ala	
360 365 370 375	
ATA ACC AAC AGC AAA GAA AGA CAC AAT TCT GTG GAG TGC TTA GAT GGA	1204
Ile Thr Asn Ser Lys Glu Arg His Asn Ser Val Glu Cys Leu Asp Gly	
380 385 390	
CTA GAT GAC ATT AGC ACA AAA CTT CCA TCG AAG CTG CAG AAA ATT ACG	1252
Leu Asp Asp Ile Ser Thr Lys Leu Pro Ser Lys Leu Gln Lys Ile Thr	
395 400 405	
GGG AGA GAA GAC TTT CCC AAA AAA CTC CTG AGG ATG AGT TCT ACA ACT	1300
Gly Arg Glu Asp Phe Pro Lys Lys Leu Leu Arg Met Ser Ser Thr Thr	

410	415	420	
TCA GAA AAA GCC TAT AGT TTG GGT GAT TTG CCC ATG AAA CTC CAA CGA			1348
Ser Glu Lys Ala Tyr Ser Leu Gly Asp Leu Pro Met Lys Leu Gln Arg			
425	430	435	
ATA AGT TCG GTT CCT GGC AAC TCT GAA GAA AAA CTG GTA TCT AAA ACC			1396
Ile Ser Ser Val Pro Gly Asn Ser Glu Glu Lys Leu Val Ser Lys Thr			
440	445	450	455
ACC AAG ATG TTA TCA GAT CCC ATG AGC CAG TCT GTG GCC GAT TTG CCA			1444
Thr Lys Met Leu Ser Asp Pro Met Ser Gln Ser Val Ala Asp Leu Pro			
	460	465	470
CCG AAG CTT CAA AAG ATG GCT GGA GGA CCT ACC AGG ATG GAA GGG AAT			1492
Pro Lys Leu Gln Lys Met Ala Gly Gly Pro Thr Arg Met Glu Gly Asn			
	475	480	485
CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GAC CGC TTC ACA			1534
Leu Pro Ala Lys Leu Arg Lys Met Asn Ser Asp Arg Phe Thr			
	490	495	500
TAGCAAACA CCCCATTAGG CATTATTTCA TGTTTTGATT TAGTTTTAGT CCAATATTTG			1594
GCTGATAAGA TAATCCTCCC CGGGAAATCT GAGAGGTCTA TCCCAGTCTG GCAAATTCAT			1654
CAGAGGACTC TTCATTGAAG TGTTGTTACT GTGTTGAACA TGAGTTACAA AGGGAGGACA			1714
TCATAAGAAA GCTAATAGTT GGCATGTATT ATCACATCAA GCATGCAATA ATGTGCAAAT			1774
TTTGCATTTA GTTTTCTGGC ATGATTTATA TATGGCATAT TTATATTGAA TATTCTGGAA			1834
AAATATATAA ATATATATTT GAAGTGGAGA TATTCTCCCC ATAATTTCTA ATATATGTAT			1894
TAAGCCAAAC ATGAGTGGAT AGCTTTCAGG GCACTAAAAT AATATACATG CATAACATACA			1954
TACATGCATA TGCACAGACA CATAACACA CATACTCATA TATATAAAAC ATACCCATAC			2014
AAACATATAT ATCTAATAAA AATTGTGATG TTTTGTTCAA AAAAAAAAAA AAAAAACTCG			2074
AG			2076

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ala	Leu	Arg	Arg	Lys	Phe	Gly	Asp	Asp	Tyr	Gln	Val	Val	Thr	1	5	10	15
Thr	Ser	Ser	Ser	Gly	Ser	Gly	Leu	Gln	Pro	Gln	Gly	Pro	Gly	Gln	Gly	20	25	30	
Pro	Gln	Gln	Gln	Leu	Val	Pro	Lys	Lys	Lys	Arg	Gln	Arg	Phe	Val	Asp	35	40	45	
Lys	Asn	Gly	Arg	Cys	Asn	Val	Gln	His	Gly	Asn	Leu	Gly	Ser	Glu	Thr	50	55	60	
Ser	Arg	Tyr	Leu	Ser	Asp	Leu	Phe	Thr	Thr	Leu	Val	Asp	Leu	Lys	Trp	65	70	75	80
Arg	Trp	Asn	Leu	Phe	Ile	Phe	Ile	Leu	Thr	Tyr	Thr	Val	Ala	Trp	Leu	85	90	95	
Phe	Met	Ala	Ser	Met	Trp	Trp	Val	Ile	Ala	Tyr	Thr	Arg	Gly	Asp	Leu	100	105	110	
Asn	Lys	Ala	His	Val	Gly	Asn	Tyr	Thr	Pro	Cys	Val	Ala	Asn	Val	Tyr	115	120	125	
Asn	Phe	Pro	Ser	Ala	Phe	Leu	Phe	Phe	Ile	Glu	Thr	Glu	Ala	Thr	Ile	130	135	140	
Gly	Tyr	Gly	Tyr	Arg	Tyr	Ile	Thr	Asp	Lys	Cys	Pro	Glu	Gly	Ile	Ile	145	150	155	160

Leu	Phe	Leu	Phe	Gln	Ser	Ile	Leu	Gly	Ser	Ile	Val	Asp	Ala	Phe	Leu
				165					170					175	
Ile	Gly	Cys	Met	Phe	Ile	Lys	Met	Ser	Gln	Pro	Lys	Lys	Arg	Ala	Glu
			180					185					190		
Thr	Leu	Met	Phe	Ser	Glu	His	Ala	Val	Ile	Ser	Met	Arg	Asp	Gly	Lys
		195					200					205			
Leu	Thr	Leu	Met	Phe	Arg	Val	Gly	Asn	Leu	Arg	Asn	Ser	His	Met	Val
	210					215					220				
Ser	Ala	Gln	Ile	Arg	Cys	Lys	Leu	Leu	Lys	Ser	Arg	Gln	Thr	Pro	Glu
225					230					235					240
Gly	Glu	Phe	Leu	Pro	Leu	Asp	Gln	Leu	Glu	Leu	Asp	Val	Gly	Phe	Ser
			245						250					255	
Thr	Gly	Ala	Asp	Gln	Leu	Phe	Leu	Val	Ser	Pro	Leu	Thr	Ile	Cys	His
		260						265					270		
Val	Ile	Asp	Ala	Lys	Ser	Pro	Phe	Tyr	Asp	Leu	Ser	Gln	Arg	Ser	Met
	275						280					285			
Gln	Thr	Glu	Gln	Phe	Glu	Val	Val	Val	Ile	Leu	Glu	Gly	Ile	Val	Glu
	290					295					300				
Thr	Thr	Gly	Met	Thr	Cys	Gln	Ala	Arg	Thr	Ser	Tyr	Thr	Glu	Asp	Glu
305					310					315					320
Val	Leu	Trp	Gly	His	Arg	Phe	Phe	Pro	Val	Ile	Ser	Leu	Glu	Glu	Gly
			325						330					335	
Phe	Phe	Lys	Val	Asp	Tyr	Ser	Gln	Phe	His	Ala	Thr	Phe	Glu	Val	Pro
		340						345					350		
Thr	Pro	Pro	Tyr	Ser	Val	Lys	Glu	Gln	Glu	Glu	Met	Leu	Leu	Met	Ser
		355					360					365			
Ser	Pro	Leu	Ile	Ala	Pro	Ala	Ile	Thr	Asn	Ser	Lys	Glu	Arg	His	Asn
	370					375					380				

Ser Asp Arg Phe Thr
500